

SEQUENCE LISTING

<110> Cahoon, Rebecca E..
Fang, Yiwen
Odell, Joan
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

<130> BB1294 US NA

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<150> 60/110,609
<151> 1998-December-02

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attgtaccct ctgtccaact aactttcccn cggcacataa acgtcggctg accttnacaa 720
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 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala
 35 40 45
 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60
 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly
 65 70 75 80
 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp
 85 90 95
 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys
 100 105 110
 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys
 115 120 125
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 130 135 140
 Asp Asp Tyr Trp Val His Asn Pro Thr Pro Thr Thr Ser
 145 150 155

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Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser
35 40 45
Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly
50 55 60
Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg
65 70 75 80
Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr
85 90 95
Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala
100 105 110
Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Ser Leu
115 120 125
Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys
130 135 140
Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys
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Glu Leu Lys

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ggcgcgtgac caccgagagc tgagcggcga cgaggactcc gtggtggcgg ccggagacct 180

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caccagcan ctcaatgcaa ctcaaagcan cgctcaagga ctcagcgcta atctggatgc 540
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Val Ala Ala Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp
      20          25          30

Met Leu Leu Val Asn Tyr Val Ala Ala His Gly Glu Gly Arg Trp Asn
      35          40          45

Ala Leu Ala Arg Cys Ala Gly Leu Arg Arg Thr Gly Lys Ser Cys Arg
      50          55          60

Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile
      65          70          75          80

Thr Ala Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly
      85          90          95

Asn Arg Trp Ser Xaa Ile Ala Gln His Leu Gln Gly Gln Arg Gln Arg
      100          105          110

Xaa Xaa Asn Tyr Trp Arg Thr Gly
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 20 25 30
 Ala Ala Gly Leu Lys Arg Thr Gly Lys Xaa Cys Arg Leu Arg Trp Xaa
 35 40 45
 Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu
 50 55 60
 Gln Leu Leu Ile Ser Thr Ser His
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<400> 9

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cagcaaggct gctgcttgct tcccggccgc cgtagcggtc gacgaggagc acggccacca 180
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<212> PRT

<213> Zea mays

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      20              25              30

His His Ser His Gln Leu Lys Gly Gly Ala Gln Glu Glu Ala Glu Asn
 35              40              45

Asp Asn Asn Lys Pro Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu
 50              55              60

Asp Leu Thr Leu Val Asn Tyr Ile Ala Asp Asn Gly Glu Gly Arg Trp
 65              70              75              80

Asn Asn Leu Ala Arg Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys
      85              90              95

Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn
 100             105             110

Phe Ser Ala Asp Glu Gln Leu Leu Ile Leu Asp Leu His Thr Arg Trp
 115             120             125

Gly Asn Arg Trp Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp
 130             135             140

Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys
 145             150             155             160
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Gln Leu Asn Cys Asp Ala Asn Ser Lys Arg Phe Lys Asp Ala Met Arg
 165 170 175
 Tyr Leu Trp Met Pro His Leu Ala Asp Asp Val Asp Thr Ile Ala Ala
 180 185 190
 Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val
 195 200 205
 Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala
 210 215 220
 Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln
 225 230 235 240
 Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp
 245 250 255
 Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn
 260 265 270
 Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln
 275 280 285
 Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser
 290 295 300
 Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln
 305 310 315 320
 Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser
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 <213> Oryza sativa

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 ctcaaaca 488

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 <212> PRT
 <213> Oryza sativa

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Ser Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg
20 25 30

Gly Arg Met Ser Pro Glu Glu Glu Arg Met Val Val Gln Leu His Ala
35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg
50 55 60

Thr Asp Asn Glu Ile Lys Asn
65 70

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<213> Oryza sativa

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Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
35 40 45
Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu Glu
50 55 60
Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg
65 70 75 80

Ile	Ala	Lys	Ser	Ile	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr			
				85					90					95				
Trp	Arg	Thr	His	Leu	Arg	Lys	Leu	Lys	Leu	Lys	Gln	Gln	Lys	Gln	Gln			
			100					105					110					
Gln	Ser	Asp	Asp	His	His	Asn	Asp	Asn	Asp	Asp	Asp	Asp	Asp	Arg	Asn			
		115					120					125						
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asn	Ser	Asn	Ser	Asn	Leu	Gln	Gln			
		130					135					140						
Gln	Pro	Gln	Pro	Glu	Asp	Glu	Ser	Ser	Ala	Ser	Gly	Ser	Leu	Gln	Ala			
145					150					155					160			
Gln	His	His	Glu	Asp	Gln	His	Gln	Leu	Phe	Leu	His	Pro	Leu	Trp	Asn			
			165						170					175				
Asp	Asp	Ile	Ile	Val	Asp	Val	Asp	Cys	Trp	Ser	Ser	Ser	Thr	Asn	Val			
		180						185					190					
Val	Ala	Pro	Pro	Pro	Met	Pro	Ala	Ser	Pro	Leu	Trp	Asp	Ile	Asp	Asp			
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Ala	Phe	Phe	Cys	Ser	Asp	Tyr	Ser	Leu	Pro	Leu	Trp	Gly						
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<220>
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 acatcccaag cccaatatg gtgacagtga gagaggagat gcgcaaggga ccatggacag 180
 agcaggagga cctgcaactg gtatgcactg tccgcctgtt cggtgaccgc cggtgggatt 240
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 <213> Oryza sativa

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 20 25 30

Trp Asp Phe Val Ala Lys Val Ser Gly Leu Arg Gly Leu Asn Arg Thr
 35 40 45

Gly Lys Ser Cys Arg Leu Arg Trp Val Asn Xaa Leu Gln Pro
 50 55 60

<210> 17
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<220>
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 cgtcaactac atcgccgccc atggcgaggg ccgctggaac gcgctcgcg cgtgcgccgg 180
 gctgaagcgg acggggaaga gctgccggct gcggtggctg aactacctga ggccggacgt 240
 gaggaggggg aacatgacgg cggaggagca gctgctgata ctggagctcc atgggcggtg 300
 ggggaatcgg tggagcaaga tcgcgagca tctccccggc cgcaccgaca acgagatcaa 360
 gaactactgg cgcacccgcg tccagaagca cgccaagcac ctcaactgcg acgtcaactc 420
 ccagcagttc aaggaccta tgcgctacct ctggatgcc gcctcctcga acgcatcaac 480
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 cactcgactc tctcacgcca taacgccgct cgcattgncga annacan 587

<210> 18
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 <213> Oryza sativa

<400> 18
 Met Met Met Ala Arg Glu Val Ser Ser Glu Glu Glu Ala Gly Gly Gly
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Asp Glu Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu Leu
 20 25 30

Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala
 35 40 45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu
 65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp
 85 90 95

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys
115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met
130 135 140

Pro
145

<210> 19
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<212> DNA
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tcccgatggg gcaaccgatg gtccaagata gcacaacatt tgcctgggag gaccgacgac 180
gagatcaaga actactggag gaccagagtg caaaagcatg ccaagcaact caattgtgat 240
gtcaacagca agaggttcaa ggatgccatg aagtacctat ggatgcctcg ccttgccgag 300
cgcatccatg ccagggctgg cgctgttgat gatagcggag actacagcaa caacgactta 360
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atggtgacta gctcatcctc 440

<210> 20
<211> 146
<212> PRT
<213> Oryza sativa

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20 25 30

Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser
35 40 45

Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn
50 55 60

Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp
65 70 75 80

Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro
85 90 95

Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser
100 105 110

Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met
115 120 125

Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser
130 135 140

Ser Ser
145

<210> 21
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tctatccgat caatcgactg gcccgcgagg atcgatcgag actcgaaagg gagggatttt 180
gatccggatc ggctcgacgat ggacatggcg cacgagaggg acgagagcag cgaggaggag 240
gtgatgggcg gcgacctgcg tcgcgggccg tggacggtgg aggaggacct cctgctcgtc 300
aactacatcg ccgcgcacgg cgaggggccg tggaaactcg tcgcccgatc agcanggctg 360
aaacgcacag gcaagagctg ccggctccgg tggctgaact acctccgcc cgacctccgg 420
cgaggcaaca tcacgccgca agagcagctg ctcatcctgg agctgcactc gcggtgggga 480
aaccgctggt ccaagatngc gcagcacctc ccgggaagca ccgacaacga gatnaagaat 540
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<210> 22
<211> 115

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<213> Oryza sativa

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20 25 30
Leu Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ser Leu
35 40 45
Ala Arg Ser Ala Xaa Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
50 55 60
Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile Thr Pro
65 70 75 80
Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg
85 90 95
Trp Ser Lys Xaa Ala Gln His Leu Pro Gly Ser Thr Asp Asn Glu Xaa
100 105 110

Lys Asn Thr
115

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 gggggccatgg acgccggagg aggacctgat gctgggtctcc tacatccagg agcacggcgc 180
 cggcaactgg cgcgccgtgc cgacgaacac cgggctgatg cgttgagca agagctgccg 240
 gctccggtgg acgaactacc tcaggccggg gatcaagcgg gggaacttca ccgagcanga 300
 ggagaagctc atcgtccacc tccaggctct cctcggcaac cgggtgggcaa cgatnncgtc 360
 gtacttgccg gganangacg ncaacnacat cangaatact gggaacannc acctcangaa 420
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<210> 24
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 <213> Oryza sativa

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Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
 20 25 30

Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
 35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Xaa Glu Glu Lys Leu Ile Val His
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Thr Xaa Xaa Ser Tyr Leu
85 90 95

Pro Gly Xaa Asp Xaa Asn Xaa Ile Xaa Asn Thr Gly Asn Xaa His Leu
100 105 110

Xaa Lys Asn Ser Arg Xaa Cys Lys Pro Pro Glu Val Xaa Lys
115 120 125

<210> 25
<211> 1427
<212> DNA
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tgaagaaggg gccatggacg ccggaggagg acctgatgct ggtctcctac atccaggagc 180
acggcgccgg caactggcgc gccgtgccga cgaacaccgg gctgatgcgt tgcagcaaga 240
gctgccggct ccggtggacg aactacctca ggccggggat caagcggggg aacttcaccg 300
agcaggagga gaagctcatc gtccacctcc aggctctcct cggcaaccgg tgggcagcga 360
tagcgtcgta cttgccggag aggacggaca acgacatcaa gaactactgg aacacgcacc 420
tcaagaagaa gctcaagaag atgcaggccg ccggagggtg ggaagacagc ggcgccgcct 480
cggaggggtg cggcgccgcg ggcgacggcg acggcgggcg gaaaagcgtg aaggccggcg 540
cacctaaggg gcagtgggag cggcggtctg agacggacat ccacacggcg cggcaggcgc 600
tgcgcgacgc gctctcgctc gaccaccccg acccgctcgc ggcgacggcg gcggcgggcg 660
cgacgccagc ggggtcgtcg gcggcggtac cgtcgagcgc ggacaacatc gcgcggctgc 720
tgaggggctg gatgcgcccg ggcgggcgcg gcggcgggcaa cggcaagggc cccgaggcgt 780
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cgccggagtg ctcgacggag acgagcaaga tggccaccgg cggcgggcgc ggcgggccccg 960
cgccggcggt ctcgatgctg gagagctggc tgctcgacga cggcgggcat gggctcatgg 1020
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taattagtct ctctgatgat gctaggggtt ggaactgac atatgtaagt taatttatac 1320
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<210> 26
<211> 323
<212> PRT
<213> Oryza sativa

<400> 26
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Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
20 25 30
Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
35 40 45
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Gln	Glu	Glu	Lys	Leu	Ile	Val	His	
65					70				75						80	
Leu	Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Ala	Ile	Ala	Ser	Tyr	Leu	
				85					90					95		
Pro	Glu	Arg	Thr	Asp	Asn	Asp	Ile	Lys	Asn	Tyr	Trp	Asn	Thr	His	Leu	
			100					105					110			
Lys	Lys	Lys	Leu	Lys	Lys	Met	Gln	Ala	Ala	Gly	Gly	Gly	Glu	Asp	Ser	
		115					120					125				
Gly	Ala	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Arg	Gly	Asp	Gly	Asp	Gly	Gly	
	130					135					140					
Gly	Lys	Ser	Val	Lys	Ala	Ala	Ala	Pro	Lys	Gly	Gln	Trp	Glu	Arg	Arg	
145					150				155						160	
Leu	Gln	Thr	Asp	Ile	His	Thr	Ala	Arg	Gln	Ala	Leu	Arg	Asp	Ala	Leu	
				165					170					175		
Ser	Leu	Asp	His	Pro	Asp	Pro	Ser	Pro	Ala	Thr	Ala	Ala	Ala	Ala	Ala	
			180					185					190			
Thr	Pro	Ala	Gly	Ser	Ser	Ala	Ala	Tyr	Ala	Ser	Ser	Ala	Asp	Asn	Ile	
		195					200					205				
Ala	Arg	Leu	Leu	Gln	Gly	Trp	Met	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Gly	
	210					215					220					
Asn	Gly	Lys	Gly	Pro	Glu	Ala	Ser	Gly	Ser	Thr	Ser	Thr	Thr	Ala	Thr	
225					230					235					240	
Thr	Gln	Gln	Gln	Pro	Gln	Cys	Ser	Gly	Glu	Gly	Ala	Ala	Ser	Ala	Ser	
				245					250					255		
Ala	Ser	Ala	Ser	Gln	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Thr	Ala	Gln	Thr	
			260				265						270			
Pro	Glu	Cys	Ser	Thr	Glu	Thr	Ser	Lys	Met	Ala	Thr	Gly	Gly	Gly	Ala	
		275					280					285				
Gly	Gly	Pro	Ala	Pro	Ala	Phe	Ser	Met	Leu	Glu	Ser	Trp	Leu	Leu	Asp	
	290					295					300					
Asp	Gly	Gly	Met	Gly	Leu	Met	Asp	Val	Val	Pro	Leu	Gly	Asp	Pro	Ser	
305					310					315					320	
Glu	Phe	Phe														

<210> 27
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 <212> DNA
 <213> Glycine max

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<400>  27
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aaaacaactg tgcaacacgt ctcaagatcc tgaagtgaga aaaggacctt ggacgatgga 120
agaagacttg atcttngatc aactatattg caaatcatgg ggaaggtggt tggaattctt 180

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tggccaaaag ctgctggtct caaacgtacc ggaaagattg ccggctaang tggctaaact 240
acctccgtcc tgatgttaga agagggaata ntacacccga aggaacaact ttgatcatgg 300
agcttcacgc aaagtgggga aacaggtggt ccaaaattgc caagcatcta cctggtagga 360
cagtaatgag atnaagaact antggnggac aaggatcaga agcacatcaa gcaactgaga 420
attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480
ggtgaaccat ggnnactatc ccaacctttt naaggaagtn angcatttct naatcnttcc 540
ccaaataacc gnntatc 557

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<210> 28
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<212> PRT
<213> Glycine max

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<400> 28
Ser Gln Asp Pro Glu Val Arg Lys Gly Pro Trp Thr Met Glu Glu Asp
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Leu Ile Xaa Xaa Ile Asn Tyr Ile Ala Asn His Gly Glu Gly Val Trp
          20          25          30
Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys
          35          40          45
Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn
          50          55          60
Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp
          65          70          75          80
Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr
          85          90

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<210> 29
<211> 988
<212> DNA
<213> Glycine max

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<400> 29
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acgatggaag aagacttgat cttgatcaac tatattgcaa atcatgggga aggtgttttg 180
aattcttttg ccaaagctgc tgggtctcaa cgtaccggaa agagttgccg gctaaggttg 240
ctaaactacc tccgtcctga tggtagaaga gggaatatta cccccgagga acaacttttg 300
atcatggagc ttcacgcaaa gtgggggaaac aggtggtcca aaattgcca gcatctacct 360
ggtaggacag ataatgagat caagaactat tggaggacca ggatccagaa gcacatcaag 420
caagctgaga actttcagca acaaatcagc aataactctg agataaatga tcaccaagct 480
agcactagcc atgtttctac catggctgaa cccatggaga cctattctcc acccttttat 540
caaggaatgt tagagccatt ttcttcaatt cagttcccca caattaatcc tgatcaatcc 600

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agttgttgta ccaatgacaa caacaacagc attaactatt ggagcatgga ggatatctgg 660
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ttatataagt agttggatat gtttggtttt gcgtaccatt attagcatat atatatatat 840
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gtttgcttaa aaaaaaaaaa aaaaaaaaaa 988

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<210> 30
<211> 208
<212> PRT
<213> Glycine max

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<400> 30
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 1              5              10              15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile
      20              25              30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
      35              40              45

Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
 50              55              60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
 65              70              75              80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
      85              90              95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
      100              105              110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
      115              120              125

Ile Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
      130              135              140

Val Ser Thr Met Ala Glu Pro Met Glu Thr Tyr Ser Pro Pro Phe Tyr
      145              150              155              160

Gln Gly Met Leu Glu Pro Phe Ser Ser Ile Gln Phe Pro Thr Ile Asn
      165              170              175

Pro Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ser Ile Asn
      180              185              190

Tyr Trp Ser Met Glu Asp Ile Trp Ser Met Gln Leu Leu Asn Gly Asp
      195              200              205

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<210> 31
<211> 530
<212> DNA
<213> Glycine max

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 <222> (522)

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 tggaaactctt tggccaaggc tgctggactt aaacgtaccg gaaagagttg ccggctccgg 180
 tggctaaact acctccgtcc tgatgttaga agagggaata ttacacccga ggaacagctt 240
 ttgatcatgg aacttcatgc aaagtgggga aacaggtggt ccaaaattgc caagcatcta 300
 nccggaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacanctca 360
 agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420
 cttgcacaac caattgtcaa caatgggcaa cccaaaaaaa ctaatctcan caatttcaag 480
 gaagnttatt cattnaatca attccaaaaa ccncacntct antgtttcaa 530

<210> 32
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 32
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			20					25					30			
Asn	His	Gly	Glu	Gly	Val	Trp	Asn	Ser	Leu	Ala	Lys	Ala	Ala	Gly	Leu	
		35					40					45				
Lys	Arg	Thr	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Leu	Asn	Tyr	Leu	Arg	
	50					55					60					
Pro	Asp	Val	Arg	Arg	Gly	Asn	Ile	Thr	Pro	Glu	Glu	Gln	Leu	Leu	Ile	
	65				70					75					80	
Met	Glu	Leu	His	Ala	Lys	Trp	Gly	Asn	Arg	Trp	Ser	Lys	Ile	Ala	Lys	
				85					90					95		
His	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Arg	Thr	
			100					105					110			
Arg	Ile	Gln	Lys	His	Leu	Lys	Gln	Ala	Ser	Ser	Ser	Phe	Gln	Gln	Gln	
		115					120					125				
Ser	Ser	Asn	Ser	Glu	Ile	Ile	Tyr	His	Pro	Gln	Ala	Cys	Thr	Ser	Gln	
	130					135					140					
Val	Ser	Thr	Met	Ala	Gln	Pro	Ile	Glu	Thr	Tyr	Ser	Pro	Pro	Ser	Tyr	
	145				150					155					160	
Gln	Gly	Met	Leu	Asp	Pro	Phe	Ser	Ile	Gln	Phe	Pro	Thr	Asn	Pro	His	
				165					170					175		
His	Ser	Ser	Cys	Cys	Thr	Asn	Asp	Asp	Asp	Asn	Asn	Asn	Tyr	Trp	Ser	
			180					185					190			
Met	Glu	Asp	Ile	Trp	Ser	Met	Gln	Leu	Ala	Asn	Tyr					
		195					200									

<210> 33
 <211> 910
 <212> DNA
 <213> Glycine max

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 <222> (798)

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 aactatattg caaatcacgg tgaagggtgt tgggaattctt tagccaaagc ttctgggtctt 180
 aaacgaacgg gaaagagttg tgcactccgt tggctaaact accttcgtcc tgatgttaga 240
 agaggaaaca ttacacccga agaacagctt ttgatcatag aacttcatgc aaagtggggc 300
 aataggtggt ccaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360


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ttctggagaa ctaggatcca gaagcacatt aagcaagctg agacttcaca acaacatggt 420
aattcatcag agaatagtaa taatgatcat caagcaagca atagcactag caaggtgtcc 480
accatggcac atccaaatga gactttctct tcaccctcat accaagcaac ttttgagcca 540
tttcaacctc aattcctaca atcaatgatc aatcaagttg ttgtaccagc aacaacaact 600
attggagcat cgaggatatc tggtcgtcta tgcaattact caatggagat waattaaatc 660
tagctatatg catgcttata taaatcatat atgtgatgat atataaacct aagctcttat 720
tgagtgtggt caggcttaat aacatcatta ggtctggtat atatgagtag gttaagattg 780
gtgtgcatgc ctaaatgnag tattgcntta ttgnagtaag aataactagt tatggatgcc 840
tttaaaaaaa agtttagttat gaattgaaat atatatgaac ttatatata aaaaaaaaaa 900
aaaaaaaaaa                                     910

```

```

<210> 34
<211> 206
<212> PRT
<213> Glycine max

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```

<400> 34
Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
 1                               5                               10                               15

Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
                20                               25                               30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
                35                               40                               45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50                               55                               60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
 65                               70                               75                               80

Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
                85                               90                               95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
                100                               105                               110

Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly
                115                               120                               125

Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr
                130                               135                               140

Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro
145                               150                               155                               160

Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser
                165                               170                               175

Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser
                180                               185                               190

Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn
                195                               200                               205

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<210> 35
<211> 863
<212> DNA
<213> Glycine max

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<400> 35
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agatcctgaa gtgagaaaaag ggccttggac aatggaagaa gacttgatct tgatgaacta 120
tattgcaa at catggggaag gtgtttggaa ctctttggcc aaagctgctg gtctcaaacg 180
taacggaa ag agttgccggc taaggtggct aaattacctc cgtcctgatg ttagaagagg 240
gaatattaca cccgaggaac aacttttggat tatggagctc cacgcaaagt ggggaaacag 300
gtggtccaaa attgccaagc atctacctgg aaggactgat aatgagatca agaactattg 360
gaggacaagg atccagaagc acatcaagca agctgagAAC tttcagcaac agagtagtaa 420
taattctgag ataaatgatc accaagctag cactagccat gtttccacca tggctgagcc 480
catggagatg tattctccac cctgttatca aggaatgtta gagccatttt caactcagtt 540
ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaaa tattatcaag 660
ataaaaccta agttytgaag ttccataagg ctggaatgtc tytgattaa aacatattat 720
tgggtttgtt tatataagta gttggatgtt tgggttttgcg taccattatt agctatgtgc 780
tgtaatatat acgagatytt atattaaact atatctgcat gctttatata taaaaaaaaa 840
aaaaaaaaa aaaaaaaaaa aaa 863

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```

<210> 36
<211> 206
<212> PRT
<213> Glycine max

```

```

<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
 1 5 10 15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
 20 25 30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
 35 40 45

Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
 50 55 60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
 65 70 75 80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
 85 90 95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
 100 105 110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
 115 120 125

Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
 130 135 140

Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr
 145 150 155 160

Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro
 165 170 175

Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ile Asn Tyr Trp
 180 185 190

```

Ser Met Glu Asp Ser Trp Ser Met Gln Leu Leu Asn Gly Asp
 195 200 205

<210> 37
 <211> 805
 <212> DNA
 <213> Glycine max

<400> 37
 aaaaaaacat gcaactcatc atctcatgat cctgaagtga gaaagggacc atggaccatg 60
 gaagaagact tgatcttgat aaactatat gcaaatacac gtgaagggtg ttggaactcc 120
 ttagccaaag cttctggtct caaacgaacg ggaaagagtt gtcgactccg ttggctaaac 180
 taccttcgtc ctgatgttag aagaggaaac attacacccg aggaacagct tttgatcata 240
 gaacttcatg caaagtgggg caatagggtg tccaaaattg caaagcatct tccaggaaga 300
 actgacaatg agattaagaa cttctggaga acaaggatcc aaaagcacat taagcaagct 360
 gagacttcac aacaacatgg taattcagag aataatgatc atcaagcaag cactagtact 420
 agcaaagtgt ccacatggc acatccaaat gagactttct ctccaccctc ataccaagga 480
 acttttgagc cattccaacc tcaattccct acaatcactg atcaatcaag ttgttgtacc 540
 accaccaacg acaacaacaa ctattggagc atcgaggata tctggtcgtc tatgcaatta 600
 ctcaatggag attaaaccta gctatatgca tgcctatata aatcatatat atgatgatat 660
 ataaacctaa gctctttagt agtgtgttca ggcttaataa catcattagg tctgtttata 720
 tgagtagtct aagtttggtg tttgtaatgc atgatgtgag ttaagaatta atttagttat 780
 ggttggaaaa aaaaaaaaaa aaaaa 805

<210> 38
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 38
 Lys Lys Pro Cys Asn Ser Ser Ser His Asp Pro Glu Val Arg Lys Gly
 1 5 10 15
 Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala Asn
 20 25 30
 His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu Lys
 35 40 45
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 50 55 60
 Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile Ile
 65 70 75 80
 Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys His
 85 90 95
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Arg
 100 105 110
 Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly Asn
 115 120 125
 Ser Glu Asn Asn Asp His Gln Ala Ser Thr Ser Thr Ser Lys Val Ser
 130 135 140
 Thr Met Ala His Pro Asn Glu Thr Phe Ser Pro Pro Ser Tyr Gln Gly
 145 150 155 160

Thr Phe Glu Pro Phe Gln Pro Gln Phe Pro Thr Ile Thr Asp Gln Ser
165 170 175

Ser Cys Cys Thr Thr Thr Asn Asp Asn Asn Asn Tyr Trp Ser Ile Glu
180 185 190

Asp Ile Trp Ser Ser Met Gln Leu Leu Asn Gly Asp
195 200

<210> 39
<211> 751
<212> DNA
<213> Glycine max

<400> 39
tggatgttaa gaaaggtggg tctgtagtac aagcacaagt gaagttgcag aagcataacg 60
aaaaggagat gggcatgaga aaaggtccat gggcgggttga ggaggacacc attctggtca 120
attacatcgc cacacacggt gaaggccact ggaattccgt ggcacgatgt gcaggtctaa 180
ggaggagtgg gaagagttgc agattaaggt ggctaaacta cttgcgcca gacgtgcggc 240
gtggaatat cacactccaa gaacaaatat taattctcga ccttcactct cgctggggca 300
acaggtggtc aaagattgct caacagctgc caggaagaac agacaacgaa ataaagaact 360
attggaggac cagagtgata aaacaagcga agcagctaaa gtgcgatgtg aatagcaaac 420
agttcagaga cacgttgctg tacgtttgga tgccgcgctt gctggagcgg cttcagccca 480
catcacaagc actggagcca aaccaaagtg gacttgtgtt acacgcttca tcatcactgc 540
ttccttcgaa ttccgaccat agtattgaaa gggggtcgga tctgtggcca ggtttcaata 600
accaaatggt gttggaacag gggagtggcg gtgacttggt ggaaagtttg tgggatgacg 660
acaatatgtg ctttttgcaa cagctttctt atgacctcca aatgaaataa aatacaattc 720
ccttccgtca cgcaaaaaaa aaaaaaaaaa a 751

<210> 40
<211> 235
<212> PRT
<213> Glycine max

<400> 40
Asp Val Lys Lys Gly Gly Ser Val Val Gln Ala Gln Val Lys Leu Gln
1 5 10 15
Lys His Asn Glu Lys Glu Met Gly Met Arg Lys Gly Pro Trp Ala Val
20 25 30
Glu Glu Asp Thr Ile Leu Val Asn Tyr Ile Ala Thr His Gly Glu Gly
35 40 45
His Trp Asn Ser Val Ala Arg Cys Ala Gly Leu Arg Arg Ser Gly Lys
50 55 60
Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg
65 70 75 80
Gly Asn Ile Thr Leu Gln Glu Gln Ile Leu Ile Leu Asp Leu His Ser
85 90 95
Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Gln Leu Pro Gly Arg
100 105 110
Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Ile Lys Gln
115 120 125

Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr
130 135 140

Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr
145 150 155 160

Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser
165 170 175

Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser
180 185 190

Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser
195 200 205

Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe
210 215 220

Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys
225 230 235

<210> 41
<211> 500
<212> DNA
<213> Glycine max

<400> 41
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cacaaaaaca ccaaccatgt ccacaattgc aaagagagat ttgagttcta atgaagaaga 120
gagtgagctg agaagaggct cttggactct tgaagaagac agcttactca tacactatat 180
tgctcgtcat ggtgaaggcc gttggaatat gttagccaaa agtgcaggat tgaagaggac 240
tggaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300
cctcactcca caggagcaac tcttgatcct tgaactccat tccaagtggg gtaacagggtg 360
gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420
aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480
ttgatgctgt cagtgttttt 500

<210> 42
<211> 229
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (138)

<400> 42
Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Glu Ser
1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile
20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys
35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu
 65 70 75 80
 Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser
 85 90 95
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
 100 105 110
 Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu
 115 120 125
 Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro
 130 135 140
 Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His
 145 150 155 160
 Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser
 165 170 175
 Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser
 180 185 190
 Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His
 195 200 205
 Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro
 210 215 220

Ile Phe Thr Ala Thr
225

<210> 43
 <211> 1348
 <212> DNA
 <213> Glycine max

<400> 43

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tagtgaggac	gagatggacc	ttcgaagagg	cccttggacc	gtcgatgaag	acctcactct	180
tatcaattac	gttgccactc	atggcgaagg	tcgctggaat	accctcgccc	tctctgctgg	240
gctgaaacga	acggggaaga	gttgcagatt	gaggtggctg	aattatctgc	gtcctgatgt	300
tcgacgtgga	aacatcacgc	ttgaagaaca	acttttgatt	ctggagctcc	attctcgctg	360
gggaaaccga	tggtcgaaaa	ttgctcaata	tttgcctggg	agaaccgaca	atgagataaa	420
gaactattgg	agaacccgtg	tccaaaagca	tgccaagcaa	ctcaaatacg	acgtgaatag	480
caagcaattc	aaggacacca	tgcgttacat	ttggatgcca	aggctcgtgg	aacgcattca	540
agccaccgct	gccgcctccg	caccacaacc	cgttaccgta	ccaccgcgac	caacaatgca	600
tacacctacg	gaagcaacct	taataacaac	aaattcgagg	ttcacgatca	caagggcaaa	660
atgggggttaa	ccgatccttc	agttatgaac	aatgacttaa	tgggttcaca	tgtcacgcaa	720
agttacaccc	ctgagaatag	tagcaccggt	gcgtcatcat	cagactcggt	tgggactcaa	780
gtctcagcaa	tttctgattt	gactgaatat	tacactgtca	ctggtagtgg	taacaataac	840
aataactaatt	ctgcggatta	ttatcaaccc	tctcaaatta	gttactcgga	tagttgcatc	900
acaagcccat	ctgggttggt	ccctcaaggg	ctagattttc	aatccatgga	tccaaacacc	960
ccgtggaaca	tgcaaagtgg	ggactcctct	gacagttttt	ggaacgttga	aagcatgttg	1020
ttcttagagc	agcaactcat	gaatgacaac	atgtgaaaac	attgggaata	ggaaaataag	1080
acttagatac	ggttcttctt	agtattgtgt	tttaattaaa	gttaaagtta	acacaagtta	1140
ttgaagtgaa	actttaattt	taattgaata	ataatactga	aaacaagagt	tgtatttaag	1200
ttttattctt	ttatgaatta	tgaattagat	tgacagaagg	ggttgtttgt	gaaatataca	1260

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1348

<210> 44
 <211> 196
 <212> PRT
 <213> Glycine max

<400> 44
 Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu
 1 5 10 15
 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
 20 25 30
 Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr
 35 40 45
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
 50 55 60
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
 65 70 75 80
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
 85 90 95
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
 100 105 110
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
 115 120 125
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile
 130 135 140
 Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser
 145 150 155 160
 Ala Pro Gln Pro Val Thr Val Pro Pro Arg Pro Thr Met His Thr Pro
 165 170 175
 Thr Glu Ala Thr Leu Ile Thr Thr Asn Ser Arg Phe Thr Ile Thr Arg
 180 185 190
 Ala Lys Trp Gly
 195

<210> 45
 <211> 1236
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (519)

<220>
 <221> unsure
 <222> (521)

<220>
 <221> unsure
 <222> (530)..(531)

<220>
 <221> unsure
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<220>
 <221> unsure
 <222> (800)

<220>
 <221> unsure
 <222> (1124)

<220>
 <221> unsure
 <222> (1151)

<400> 45
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 gcaacaccct ttttaagttgt gaggacgaga tggaccctcg aagaggccct tggaccgtcg 180
 atgaagacct cactcttata aattacattg ccactcatgg cgaaggctcg tggaacacgc 240
 tcgccctctc tgctgggctg aaacgaacgg ggaagagttg cagattgagg tggctgaatt 300
 atctgcgtcc tgatgttcga cgtggaaaca tcacacttga agaacaactt ttgattctgg 360
 agcttcattc tcgctgggga aaccgttggg cgaaaattgc tcaatatttg cctggtagaa 420
 ccgacaacga gataaagaac tattggagaa cccgtgtcca aaagcatgcc aagcaactca 480
 aatgtgacgt gaatagcaag caattcaagg acaccatgng ntacctttgn natnccaagg 540
 ctggtggaac gcattcaagc agcggcgacg gcccccgtaa ccaccaccgt aactgcggcc 600
 gccaccaaca atgcattcac ctacgggraac aaccttatac caccaaattc gaggttctga 660
 atcacaaggg cagaatgggg ttaaccgatc cttcagttgc gaacaatgac tttgtgggtt 720
 cacatgtcac gcaaaggtag cctactcctg agaatagtag cacgggtgcg tcatcatcag 780
 actcgtttgg gactcaagtn tcaacaattt ctgatttgac tgaaaattcc agtgtccctg 840
 aaaatactaa ttctgcggat tattatcaac cctctcaaat tagtaattac tcggataatt 900
 gcatcacaag cccatctggg ttcttggtcc ctcaaggact agatcttcaa tccatggatc 960
 caaacacacc gtggaacatg caaagtgggg actcctctga caatttttgg gacgttgaaa 1020
 gcatgttatt cttagagcag caactcatga atgacaacat gtgaaacatt gggaatagga 1080
 aaataagact tagatacggg tcttctaata ttttttagtg ktgngtttta attaaagtta 1140
 aagttaacac nagttattga agtgaaactt taattttaat taaataataa tcctgaaaaa 1200
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1236

<210> 46
 <211> 322
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (142)

<220>
 <221> UNSURE
 <222> (145)..(146)..(147)

<220>
 <221> UNSURE
 <222> (178)

<400> 46

Met	Asp	Glu	Lys	Gly	Ala	Arg	Ser	Ser	Asn	Thr	Leu	Leu	Ser	Cys	Glu	1	5	10	15
Asp	Glu	Met	Asp	Leu	Arg	Arg	Gly	Pro	Trp	Thr	Val	Asp	Glu	Asp	Leu	20	25	30	
Thr	Leu	Ile	Asn	Tyr	Ile	Ala	Thr	His	Gly	Glu	Gly	Arg	Trp	Asn	Thr	35	40	45	
Leu	Ala	Leu	Ser	Ala	Gly	Leu	Lys	Arg	Thr	Gly	Lys	Ser	Cys	Arg	Leu	50	55	60	
Arg	Trp	Leu	Asn	Tyr	Leu	Arg	Pro	Asp	Val	Arg	Arg	Gly	Asn	Ile	Thr	65	70	75	80
Leu	Glu	Glu	Gln	Leu	Leu	Ile	Leu	Glu	Leu	His	Ser	Arg	Trp	Gly	Asn	85	90	95	
Arg	Trp	Ser	Lys	Ile	Ala	Gln	Tyr	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	100	105	110	
Ile	Lys	Asn	Tyr	Trp	Arg	Thr	Arg	Val	Gln	Lys	His	Ala	Lys	Gln	Leu	115	120	125	
Lys	Cys	Asp	Val	Asn	Ser	Lys	Gln	Phe	Lys	Asp	Thr	Met	Xaa	Tyr	Leu	130	135	140	
Xaa	Xaa	Xaa	Lys	Ala	Arg	Gly	Thr	His	Ser	Ser	Ser	Gly	Asp	Gly	Pro	145	150	155	160
Arg	Asn	His	His	Arg	Asn	Cys	Gly	Arg	His	Gln	Gln	Cys	Ile	His	Leu	165	170	175	
Arg	Xaa	Gln	Pro	Tyr	Thr	Thr	Lys	Phe	Glu	Val	Leu	Asn	His	Lys	Gly	180	185	190	
Arg	Met	Gly	Leu	Thr	Asp	Pro	Ser	Val	Ala	Asn	Asn	Asp	Phe	Val	Gly	195	200	205	
Ser	His	Val	Thr	Gln	Arg	Tyr	Pro	Thr	Pro	Glu	Asn	Ser	Ser	Thr	Gly	210	215	220	
Ala	Ser	Ser	Ser	Asp	Ser	Phe	Gly	Thr	Gln	Val	Ser	Thr	Ile	Ser	Asp	225	230	235	240
Leu	Thr	Glu	Asn	Ser	Ser	Val	Pro	Glu	Asn	Thr	Asn	Ser	Ala	Asp	Tyr	245	250	255	
Tyr	Gln	Pro	Ser	Gln	Ile	Ser	Asn	Tyr	Ser	Asp	Asn	Cys	Ile	Thr	Ser	260	265	270	
Pro	Ser	Gly	Phe	Leu	Phe	Pro	Gln	Gly	Leu	Asp	Leu	Gln	Ser	Met	Asp	275	280	285	
Pro	Asn	Thr	Pro	Trp	Asn	Met	Gln	Ser	Gly	Asp	Ser	Ser	Asp	Asn	Phe	290	295	300	

Trp Asp Val Glu Ser Met Leu Phe Leu Glu Gln Gln Leu Met Asn Asp
 305 310 315 320

Asn Met

<210> 47
 <211> 1181
 <212> DNA
 <213> Glycine max

<400> 47
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 atttttaatc atggggaagg gcgatggaat ttgctggcta aacgttcagg attaaagaga 180
 actgggaaaa gttgcagatt aaggtggcta aattatctaa agccagatgt aaaacgggga 240
 aatttaaccc cacaagagca acttataatt cttgaactcc actcaaagtg gggaaacagg 300
 tgggtcaaaaa ttgcacaaca tttgccaggc agaacagaca atgaaatcaa gaactattgg 360
 agaactagga ttcagaaaca agcaagacat ttgaaaattt aacttgacag cagagagttt 420
 caagaacttg ttaggcgttt ctggatgcct agattgcttc agaaagcaaa agaatcatct 480
 tcttcaaaca tgtcaattca aaaccaggca attcctatgc cttttgatta tgtttctcag 540
 catttaactg ttgggaccat acctccttgg cagggacctt gtatgaatga agctgggtccc 600
 acttacatgg accaacatga gcagactcag actcggaaca ccaacaatgg ttcatgcatc 660
 tccttgtctg agtcagcaaa tattccaaaa gtgcctcagc attttggaca caccaccatc 720
 acccaatttc atgccttgaa taccaatgac tttggcacct tcacatatga aggttataat 780
 gtaaacaaca atgtctatga gatggacaac ttcaaaacga ctactacatg ggtggctgag 840
 gatgcgcaat acccaatttg tgattgtcaa atggtaggaa gcaattgggt aaacaacgat 900
 tttgcatgta acatgtggaa catggatgaa ctgtggcagt ttagcaagtt acaaaaataa 960
 gatttttaggg ttttggtttt tttggaataa ccaaaagtcc aaaactcttt ctttgatgac 1020
 gttattattg ttatcatgaa ctgtggatta gctaccgaat taattaatac agatggcgat 1080
 tgttttctgt acatctgtct tgtattactc tgttcagata agtacttttg taatttgtat 1140
 tgattgagaa aagtcattaa ttagtcacta gtacaaaaaa a 1181

<210> 48
 <211> 312
 <212> PRT
 <213> Glycine max

<400> 48
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
 1 5 10 15
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
 20 25 30
 Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
 35 40 45
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
 50 55 60
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
 65 70 75 80
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
 85 90 95
 Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr
 115 120 125
 Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
 130 135 140
 Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Asn Met Ser Ile Gln
 145 150 155 160
 Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr
 165 170 175
 Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly
 180 185 190
 Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn
 195 200 205
 Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val
 210 215 220
 Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn
 225 230 235 240
 Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn
 245 250 255
 Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Thr Trp Val Ala
 260 265 270
 Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn
 275 280 285
 Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu
 290 295 300
 Trp Gln Phe Ser Lys Leu Gln Lys
 305 310

<210> 49
 <211> 1186
 <212> DNA
 <213> Glycine max

<400> 49
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 tagtcatgga gaagggcgat ggaatttgct agctaaacgt tcaggattaa agcgaactgg 180
 gaaaagttgc agattaaggt ggctaaatta tctaaagcca gatgtaaaac ggggaaattt 240
 aaccccacaa gagcaactta taatcctcga actccactca aagtggggaa acaggtggtc 300
 aaaaattgca caaaatttgc caggcagaac agacaatgaa atcaagaact attggagaac 360
 taggattcag aaacaagcaa gacatttgaa aattgacact gacaccagag agtttcagga 420
 acttgttagg cgttttctgga tgcttagatg cttcaaaaag cccaagaatc atcttcttca 480
 gccatgtcaa ttcaaaacca ggcaactcct atgccttttg atgggtgtttc tcagcattca 540
 actgttgga ccataccatc acattcacac accccttggc agggaccttg tatgaatgaa 600
 gctgggtcca cttacatgga ccaacatgag cagaactcag actctgaaca caacaatgg 660
 tcatgcatct ccttgtctga gtcagcaaat tttccaaaag tgcctcagca ttttggacgc 720
 accaccatca cccaatatca tgccttgaat aacaatgact ttggcacctt cacatatgac 780
 ggctacaatg taagcaacaa tgtctatgag atggacaact tcaaaacgcc tactacaagg 840
 gtggctgagg atgcgcaata cccaactggg gattgtcaaa tggtaggaag caattgggta 900

aacagcgatt ttgcatgtaa catgtggaac atggatgaat tgtggcaatt tagcaagtta 960
caaaaataag atttttagggt ttgggtttttt tggagttacc aagactctat ctttggtgat 1020
gttattattg ttatcatgaa ctgttgatta gctactacca aattaattaa tacagatggg 1080
gattgttttc tgtacatctg ttttgcatta ctctgttttg caatttgtat tgattgagaa 1140
aagtcattaa ttagtcacta gttcaaaaaca caaaaaaaa aaaaaa 1186

<210> 50
<211> 192
<212> PRT
<213> Glycine max

<400> 50

Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
1 5 10 15

Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
20 25 30

Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
35 40 45

Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
50 55 60

Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
65 70 75 80

Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
85 90 95

Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Asp Thr
115 120 125

Asp Thr Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
130 135 140

Cys Phe Lys Lys Pro Lys Asn His Leu Leu Gln Pro Cys Gln Phe Lys
145 150 155 160

Thr Arg Gln Leu Leu Cys Leu Leu Met Val Phe Leu Ser Ile Gln Leu
165 170 175

Leu Gly Pro Tyr His His Ile His Thr Pro Leu Gly Arg Asp Leu Val
180 185 190

<210> 51
<211> 487
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (358)

<220>
<221> unsure
<222> (429)

<400> 51
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aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180
acatgggaag accaccttgt tgtgacaaag aaggggtcaa gaaagggcct tggactcctg 240
aagaagacat catattggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300
ttcctgccaa aacaggggtg tcaagatgca gcaagagttg cagacttaga tggacgantt 360
acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420
catcttcang atcttttagg aaacagatgg ggtgcaatag cttcatacct tccacaaagg 480
acaaggg 487

<210> 52
<211> 90
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (59)

<220>
<221> UNSURE
<222> (72)

<220>
<221> UNSURE
<222> (83)

<400> 52
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
20 25 30
Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
35 40 45
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly
50 55 60
Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile
65 70 75 80
His Leu Xaa Asp Leu Leu Gly Asn Arg Trp
85 90

<210> 53
<211> 1556
<212> DNA
<213> Glycine max

<400> 53
gcacgaggag aaataaaaag agaagaaaga aaacacgata gtatcatcat atcaccacca 60
cacacataga tagagagagg aaaacgacct atattttttt tcctttgaga gcttcagggg 120
ctaggaaaat tagaaggaca gccacaagta taaaggcggg gaaataaaaag agaaagacaa 180
gaaggagaca tgggaagacc accttggtgt gacaaagaag gggcaagaa agggccttgg 240
actcctgaag aagacatcat attggtgtct tatattcagg aacatgggtc tggaaattgg 300
agggcagttc ctgccaaaac agggttgtca agatgcagca agagttgcag acttagatgg 360

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acgaattacc tgaggccagg aatcaagcgt ggtaacttca cagaacaaga ggagaagatg 420
ataatccatc ttcaagatct tttaggaaac agatgggctg caatagcttc ataccttcca 480
caaagaacag acaatgacat aaagaactat tgggaataccc atttgagaaa gaagctgaag 540
aagatgcaag caggcggtga aggtggtagc tttggagaag ggttttcagc ctcaaggcaa 600
atccctagag gccagtggga aagaaggctc caaactgata tccaaatggc aaagagagcc 660
ctcagtgaag ctctttcacc agagaaaaag ccatcttggt tatctgcctc aaactcaaac 720
ccttcagata gtagcagctc cttctcttcc acaaaaccaa caacaacaca atctgtgtgc 780
tatgcatcaa gtgctgacaa catagctaga atgctcaagg gttggatgaa gaaccacca 840
aagtcctcaa gaaccaactc gtctatgact cagaactcat tcaacaactt agcagggtgct 900
gatactgctt gtagtagtgg agcaaaggga ccactaagca gtgccgaatt gtctgagaat 960
aattttgaat ccttgtttga ttttgatcag tctttggagt cttcaaactc tgatcaattc 1020
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tgccaagaga aattagttgg ttggtgtggt gatgccaaagt ttttctaagt tgggttcatt 1200
ttgtgacata tgagactgtg ggattttttt attttatttt attttatttc ataagttata 1260
ggtagggcct catcaattaa tctcgcttcg gccttattag agagagaagt tttccagcct 1320
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tgttagttgc catacactgg caaacttgct tctcttatgt aaagttgatc ttgcgacgag 1440
atcctgcttt atggcttttag gcagcgcgac cggctcttct tctttgtgtc gcttgattag 1500
taaccccccc cgggggggggc ccgggtccaa atcccccccta atgggggtcct ttttag 1556

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<210> 54
<211> 332
<212> PRT
<213> Glycine max

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<400> 54

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Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1              5              10              15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
      20              25              30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
      35              40              45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
      50              55              60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Met Ile Ile His
 65              70              75              80

Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
      85              90              95

Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
     100              105              110

Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Gly Ser Phe
     115              120              125

Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
     130              135              140

Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
    145              150              155              160

Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
     165              170              175

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Asn	Pro	Ser	Asp	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Thr	Lys	Pro	Thr	Thr			
			180					185					190					
Thr	Gln	Ser	Val	Cys	Tyr	Ala	Ser	Ser	Ala	Asp	Asn	Ile	Ala	Arg	Met			
			195				200					205						
Leu	Lys	Gly	Trp	Met	Lys	Asn	Pro	Pro	Lys	Ser	Ser	Arg	Thr	Asn	Ser			
			210			215					220							
Ser	Met	Thr	Gln	Asn	Ser	Phe	Asn	Asn	Leu	Ala	Gly	Ala	Asp	Thr	Ala			
			225		230					235					240			
Cys	Ser	Ser	Gly	Ala	Lys	Gly	Pro	Leu	Ser	Ser	Ala	Glu	Leu	Ser	Glu			
				245				250						255				
Asn	Asn	Phe	Glu	Ser	Leu	Phe	Asp	Phe	Asp	Gln	Ser	Leu	Glu	Ser	Ser			
			260					265					270					
Asn	Ser	Asp	Gln	Phe	Ser	Gln	Ser	Leu	Ser	Pro	Glu	Ala	Thr	Val	Leu			
			275				280					285						
Gln	Asp	Glu	Ser	Lys	Pro	Asp	Ile	Asn	Ile	Ala	Ala	Glu	Ile	Met	Pro			
			290			295					300							
Phe	Ser	Leu	Leu	Glu	Lys	Trp	Leu	Leu	Asp	Glu	Ala	Gly	Cys	Gln	Glu			
			305		310				315						320			
Lys	Leu	Val	Gly	Cys	Cys	Gly	Asp	Ala	Lys	Phe	Phe							
				325					330									

<210> 55
 <211> 357
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (259)

<220>
 <221> unsure
 <222> (307)

<220>
 <221> unsure
 <222> (319)

<400> 55
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 ttgcgcaaaa gtcgcaacaa caaatgtcac ctttgctaata aactttcttc ttgcttcaac 120
 ctctgtaatc tccatgcagg cctcaaccgc acaggaaaga gctgtcgcct ccggtggggtt 180
 aactacctcc accctggggcc taaagcgtgg gcgcatgact ccccatgaaa gaacgcctca 240
 tcctccaact ccatgctcng tggggaaaca agtgggtccaa ggataacacg gaactgccaa 300
 ggcgtancga caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357

<210> 56
 <211> 54
 <212> PRT
 <213> Triticum aestivum

<220>
<221> UNSURE
<222> (21)

<220>
<221> UNSURE
<222> (27)..(28)

<220>
<221> UNSURE
<222> (41)

<400> 56
Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
1 5 10 15
Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu
20 25 30
Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys
35 40 45
Asp Asn Thr Glu Leu Pro
50

<210> 57
<211> 1072
<212> DNA
<213> Triticum aestivum

<400> 57
gcacgaggcc aaagtatcag gtttgagggg tgggggatcc aaaaattagg tagctatatt 60
gaagtatttt gcgcaaagtc gcaacaacaa atgtcacctt tgctaataac tttcttcttg 120
cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtgcgctccg 180
gtgggttaac tacctccacc ctggcctaaa gcgtggggcg atgactcccc atgaagaacg 240
cctcatcctc gagctccatg ctcggtgggg aaacagggtg tccaggatag cacggaagct 300
gccagggcgt accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360
acaggagagg aagaggagcg tgtcacccctc accatcttca tcctcagtga cataccaatc 420
cattcagcca cagacgccat cgatcatggg aattggcgag caggaacttc atgggtggcag 480
tagctgcatc acaagcatat tgaagggcac gcctgctgac atggatggat acctcatgga 540
tcagatatgg atggagattg aggcaccctc tgggggtcaac tttcatgacg ggaaggataa 600
ttcatacagc agcccctctg gccctctgct gccatcaccg atgtgggatt actacagccc 660
tgaggcaggc tggaagatgg atgagataaa gatggcccca caagttagct acagtaaagg 720
aattggcccc agttattgaa gccatatata ttgtatcaga ttactaagtt acttgcaacc 780
tagcagaagt gaaatgcttt tgttgaaaga accattagca tggatctaaa aaatatttat 840
atctatctag cattccaagt gtgctcatgt tttatgtatc tactatgtag catctagtgt 900
gcaagacatg taatgcaagg acacttccac tttgtattca caataatcag ctatctcctg 960
taagactttt ccaatgcaaa catgattagc aggtgtaata tcaacttaaa tgcttgccaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1072

<210> 58
<211> 198
<212> PRT
<213> Triticum aestivum

<400> 58
Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
1 5 10 15

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu
 20 25 30
 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg
 35 40 45
 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 50 55 60
 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val
 65 70 75 80
 Ser Pro Ser Pro Ser Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro
 85 90 95
 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly
 100 105 110
 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp
 115 120 125
 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly
 130 135 140
 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly
 145 150 155 160
 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly
 165 170 175
 Trp Lys Met Asp Glu Ile Lys Met Ala Pro Gln Val Ser Tyr Ser Lys
 180 185 190
 Gly Ile Gly Pro Ser Tyr
 195

<210> 59
 <211> 521
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (108)

<220>
 <221> unsure
 <222> (355)

<220>
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<220>
 <221> unsure
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<400> 59
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 cagcatggcg gcggagccgg aggaggaggc ggaccggagg aggaggcngg agctccggcg 120
 agggccgtgg acggtggacg aggaccttac gctgatcaac tacatcgcg accacggcga 180
 gggccgctgg aacgcgctgg cgcggggccgc cggcctgagg cgcacgggga agagctgccg 240
 gctgcggtgg ctgaactacc tccgccccga cgtgaagcgc ggcaacttca ccgccgacga 300
 gcagctcctc atcctcgacc tccactctcg ctgggggcaac cgggtggtcga agatngcgca 360
 ncacctcccg ggtcggacgg acaacgaaga tnaaagaact actgggagga ccanggtgca 420
 aaaagcacgc naancaactc aactgcnaac tccggnaanc gcaaccttta aaggatgcca 480
 ataaggtacc tctggatgcc tcgcctctca acgcatcaac c 521

<210> 60
 <211> 131
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (27)

<220>
 <221> UNSURE
 <222> (109)

<220>
 <221> UNSURE
 <222> (111)

<220>
 <221> UNSURE
 <222> (122)

<220>
 <221> UNSURE
 <222> (129)

<400> 60
 Met Asp Val Val Leu Gln Ser Arg Ser Ser Asn Ser Met Ala Ala Glu
 1 5 10 15

Pro Glu Glu Glu Ala Asp Arg Arg Arg Arg Xaa Glu Leu Arg Arg Gly
 20 25 30
 Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp
 35 40 45
 His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg
 50 55 60
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 65 70 75 80
 Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu
 85 90 95
 Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His
 100 105 110
 Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr
 115 120 125
 Xaa Val Gln
 130

<210> 61
 <211> 464
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (435)

<220>
 <221> unsure
 <222> (442)

<220>
 <221> unsure
 <222> (450)

<220>
 <221> unsure
 <222> (457)

<400> 61
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 ggcaactggc gcgccgtccc caccaggacc ggctgatgc ggtgtagcaa gagctgccgg 180
 ctccggtgga ccaactacct gcgcccaggg atcaagcgcg gcaacttcac cgaccaggag 240
 gagaagctca tcgtccacct ccaggcgctg ctcggaaca ggtgggcccgc gatcgctctc 300
 tacctccccg agcgcaccga caacgacatc aagaactact ggaacacgca actcaagcgc 360
 aagctgcaag cggggggcga cgccgcgggc aaaccggcgg cgcaaaggct gctcctctc 420
 aaagggaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62
 <211> 122
 <212> PRT
 <213> Triticum aestivum

<400> 62

Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
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Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His
20 25 30

Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His
65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
85 90 95

Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu
100 105 110

Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala
115 120

<210> 63

<211> 217

<212> PRT

<213> Pisum sativum

<400> 63

Met Asp Lys Lys Pro Cys Asn Ser Ser Gln Asp Pro Glu Val Arg Lys
1 5 10 15

Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
20 25 30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
35 40 45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
50 55 60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
65 70 75 80

Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
85 90 95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
100 105 110

Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn
115 120 125

Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His
130 135 140

Pro	His	Gln	Pro	Ser	Ser	Ser	Gln	Val	Ser	Asn	Leu	Val	Glu	Pro	Met
145					150					155					160
Glu	Thr	Tyr	Ser	Pro	Thr	Ser	Tyr	Gln	Gly	Thr	Leu	Glu	Pro	Phe	Pro
				165					170					175	
Thr	Gln	Phe	Pro	Thr	Ile	Asn	Asn	Asp	His	His	Gln	Asn	Ser	Asn	Cys
			180					185					190		
Cys	Ala	Asn	Asp	Asn	Asn	Asn	Asn	Asn	Tyr	Trp	Ser	Met	Glu	Asp	Ile
	195						200					205			
Trp	Ser	Met	Gln	Leu	Leu	Asn	Gly	Asp							
210						215									